```
      7690        7700        7710        7720        7730        7740
AATTATTGGA ATTAGATAAA TGGGCAAGTT TGTGGAATTG GTTTAACATA ACAAATTGGC

      7750        7760        7770        7780        7790        7800
TGTGGTATAT AAAAATATTC ATAATGATAG TAGGAGGCTT GGTAGGTTTA AGAATAGTTT

      7810        7820        7830        7840        7850        7860
TTGCTGTACT TTCTATAGTG AATAGAGTTA GGCAGGGATA TTCACCATTA TCGTTTCAGA

      7870        7880        7890        7900        7910        7920
CCCACCTCCC AACCCCGAGG GGACCCGACA GGCCCGAAGG AATAGAAGAA GAAGGTGGAG

      7930        7940        7950        7960        7970        7980
AGAGAGACAG AGACAGATCC ATTCGATTAG TGAACGGATC CTTAGCACTT ATCTGGGACG

      7990        8000        8010        8020        8030        8040
ATCTGCGGAG CCTTGTGCCT CTTCAGCTAC CACCGCTTGA GAGACTTACT CTTGATTGTA

      8050        8060        8070        8080        8090        8100
ACGAGGATTG TGGAACTTCT GGGACGCAGG GGGTGGGAAG CCCTCAAATA TTGGTGGAAT

      8110        8120        8130
CTCCTACAGT ATTGGAGTCA GGAACTAAAG AA.--
```

REMARKS

The above-captioned application is involved in Interference No. 102,822 with U.S. Patent Application Serial No. 693,866 of Chang et al.

New claims 116-119 are identical to Chang's proposed counts C-1 to C-4, respectively, and thus "correspond exactly" to the counts as defined by 37 C.F.R. §1.601(f).[1/]

Claim 116 finds support in applicants' specification at, e.g., original claims 5-7 and the following text:

> The invention relates to cloned DNA sequences indistinguishable from genomic RNA and DNA of lymphadenopathy-associated virus

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1/ The only difference between the claim Chang proposed be added to Alizon's involved application and Alizon's claims 116-119 is the use of the term "LAV" instead of "HTLV-III" as suggested by Chang. The term "LAV" is used in the involved Alizon application and identifies the same retrovirus as "HTLV-III".

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> (LAV), a process for their preparation and their uses. . . . The present invention further aims at providing polypeptides containing sequences in common with polypeptides encoded by the LAV genomic RNA. It relates even more particularly to polypeptides comprising antigenic determinants included in the proteins encoded and expressed by the LAV genome occurring in nature.

Applicants' specification at page 1, line 4 through page 2, line 5.

> These polypeptides can be used as diagnostic tools, particularly for the detection of antibodies in biological media, particularly in sera or tissues of persons afflicted with pre-AIDS or AIDS. . . .

Applicants' specification at page 15, lines 25-28.

Claim 117 finds support in applicants' specification at, e.g., original claim 8 as well as in the following quote from page 1 of the specification:

> The invention relates to cloned DNA sequences indistinguishable from genomic RNA and DNA of lymphadenopathy-associated virus (LAV), a process for their preparation and their uses. It relates more particularly to stable probes including a DNA sequence which can be used for the detection of the LAV virus or related viruses or DNA proviruses in any medium, particularly biological samples containing any of them.

Claim 118 finds support in applicants' specification at, e.g., original claim 9 as well as in the following language from the specification:

> These polypeptides can be used as diagnostic tools, particularly for the detection of antibodies in biological media, particularly in sera or tissues of persons afflicted with pre-AIDS or AIDS . . . . These monoclonal antibodies . . . then provide very useful tools for the identification and even determination of relative proportions of the

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different polypeptides or proteins in biological samples, particularly human samples containing LAV or related viruses.

Applicants' specification at page 15, line 25 through page 16, line 5.

Claim 119 finds support in applicants' specification at, e.g., original claim 10 as well as the language at page 16, lines 14-18 of the application:

> Finally it also relates to vaccine compositions whose active principal is to be constituted by any of the expressed antigens.

Claims 120-131 have the same form as claims 116-119, except that claims 120-131 contain additional recitations regarding the nature of the DNA sequence. Claims 120-131 find the same support in the Alizon involved application as claims 116-119. Claims 120-131 are further supported by the following passages from the Alizon et al. involved application:

> The coordinates of the successive sites of the whole LAV genome (restriction map) are indicated hereafter too, with respect to the *Hind*III site (selected as of coordinate 1) which is located in the R region. The coordinates are estimated with an accuracy of ± 200 bp:

Hind III	0
Sac I	50
Hind III	520
Pst I	800
Hind III	1,100
Bgl II	1,500
Kpn I	3,500
Kpn I	3,900
Eco RI	4,100
Eco RI	5,300
Sal I	5,500
Kpn I	6,100
Bgl II	6,500
Bgl II	7,600
Hind III	7,850
Bam HI	8,150

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Xho I	8,600
Kpn I	8,700
Bgl II	8,750
Bgl II	9,150
Sac I	9,200
Hind III	9,250

Another DNA variant according to this invention optionally contains an additional Hind III approximately at the 5,550 coordinate.

Reference is further made to fig. 1 which shows a more detailed restriction map of said whole DNA (λJ19).

An even more detailed nucleotide sequence of a preferred DNA according to the invention is shown in figs. 4-12 hereafter.

See the Alizon et al. involved application S.N. 158,652 at page 2, line 28 to page 3, line 25.

3) The envelope gene (or ORF-env)

The DNA sequence thought to code for envelope proteins is thought to extend from nucleotide position 5670 (starting with 5' AAA GAG GAG A . . . . 3') up to nucleotide position 8132 (ending by . . . . A ACT AAA GAA 3'). Polypeptide structures of sequences of the envelope protein correspond to those read according to the "phase 3" reading phase.

The start of env transcription is thought to be at the level of the ATG codon at positions 5691-5693.

Additional features of the envelope protein coded by the env genes appear on figs. 13-18. These are to be considered as paired figs. 13 and 14; 15 and 16; 17 and 18, respectively.

Alizon et al. involved application S.N. 158,652 at page 10, line 13 to line 26.

Since claims 116-131 are fully supported by applicants' disclosure and do not introduce any new matter, applicants respectfully request entry of this Amendment pursuant to 37 C.F.R. §§ 1.633(c)(2), 1.637(c)(2), and 1.115.

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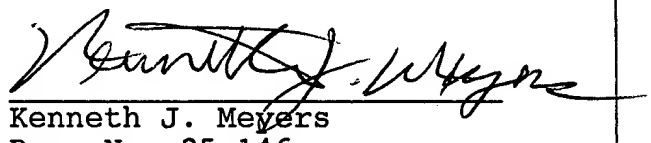
Enclosed is a check to cover the cost of the claims added by this Amendment. If there are any other fees due in connection with the filing of this Amendment, please charge the fees to our Deposit Account No. 06-0916. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for above, such an extension is requested and the fee should also be charged to our Deposit Account.

Respectfully submitted,

Date: June 21, 1993

By: 

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